

SEQ ID NO: 1

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CAAAAACAGCAACAGAAAGCAGGACGTGAGACTTCTACCTGCTCACTCAGAATCATTCT 60
GCACCAACCATGGCCACGTTTGTGGAGCTCAGTACCAAAGCCAAGATGCCCATTTGTGGGC 120
5 CTGGGCACTTGGAAGTCTCCTCTCGGCAAAGTGAAAGAAGCAGTGAAGGTGGCCATTGAT 180
GCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAATGAACATGAAGTGGGGGAA 240
GCCATCCAAGAGAAGATCCAAGAGAAGGCTGTGAAGCGGGAGGACCTGTTTCATCGTCAGC 300
AAGTTGTGGCCCACTTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAATATAAAC 360
CAGTGACTAACCAGGTTGAGTGTCAACCATACTCACGCAGGAGAACTGATCCAGTACT 420
10 GCCACTCCAAGGGCATCACCGTTACGGCCTACAGCCCCCTGGGCTCTCCGGATAGACCTT 480
GGGCCAAGCCAGAAGACCTTCCCTGCTGGAGGATCCCAAGATTAAGGAGATTGCTGCAA 540
AGCACAAAAAAACCGCAGCCCAGGTTCTGATCCGTTTCCATATCCAGAGGAATGTGATTG 600
TCATCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAACATTCAGGTCTTTGACTTTA 660
AATTGAGTGATGAGGAGATGGCAACCATACTCAGCTTCAACAGAACTGGAGGGCCTGTA 720
15 ACGTGTTGCAATCCTCTCATTGGAAGACTATCCCTTCGATGCAGAATATTGAGGTTGAA 780
TCTCCTGGTGAGATTATACAGGAGATTCTCTTTCTTCGCTGAAGTGTGACTACCTCCACT 840
CATGTCCCATTTTAGCCAAGCTTATTTAAGATCACAGTGAACCTTAGTCCTGTTATAGACG 900
AGAATCGAGGTGCTGTTTTAGACATTTATTTCTGTATGTTCAACTAGGATCAGAATATCA 960
CAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTTTTCCACTTATCTGATCAGAACAA 1020
20 ATGTTTATTAAGCATCAGAACTCTGCCAACACTGAGGATGTAAAGATCAATAAAAAAAA 1080
TAATAATCAT 1090
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SEQ ID NO: 2

	Met	Ala	Thr	Phe	Val	Glu	Leu	Ser	Thr	Lys	10
5	Ala	Lys	Met	Pro	Ile	Val	Gly	Leu	Gly	Thr	20
	Trp	Lys	Ser	Pro	Leu	Gly	Lys	Val	Lys	Glu	30
	Ala	Val	Lys	Val	Ala	Ile	Asp	Ala	Gly	Tyr	40
	Arg	His	Ile	Asp	Cys	Ala	Tyr	Val	Tyr	Gln	50
	Asn	Glu	His	Glu	Val	Gly	Glu	Ala	Ile	Gln	60
10	Glu	Lys	Ile	Gln	Glu	Lys	Ala	Val	Lys	Arg	70
	Glu	Asp	Leu	Phe	Ile	Val	Ser	Lys	Leu	Trp	80
	Pro	Thr	Ser	Arg	Ser	Arg	Ser	Ser			88

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SEQ ID NO: 3

CAAAAACAGCAACAGAAAGCAGGACGTGAGACTTCTACCTGCTCACTCAGAATCATTTCT 60
GCACCAACCATGGCCACGTTTGTGGAGCTCAGTACCAAAGCCAAGATGCCCATTGTGGGC 120
5 CTGGGCACTTGGAAGTCTCCTCTCGGCAAAGTGAAAGAAGCAGTGAAGGTGGCCATTGAT 180
GCAGGATATCGGCACATTGACTGTGCCTATGTCTATCAGAATGAACATGAAGTGGGGGAA 240
GCCATCCAAGAGAAGATCCAAGAGAAGGCTGTGAAGCGGGAGGACCTGTTTCATCGTCAGC 300
AAGTTGTGGCCCACTTTCTTTGAGAGACCCCTTGTGAGGAAAGCCTTTGAGAAGACCCTC 360
AAGGACCTGAAGCTGAGCTATCTGGACGTCTATCTTATTCACTGGCCACAGGGATTCAAG 420
10 TCTGGGGATGACCTTTTCCCAAAGATGATAAAGGTAATGCCATCGGTGGAAGCAACG 480
TTCTTGATGCCTGGGAGGCCATGGAGGAGCTGGTGGATGAGGGGCTGGTGAAAGCCCTT 540
GGGGTCTCCAATTTAGCCACTTCCAGATCGAGAAGCTCTTGAACAAACCTGGACTGAAA 600
TATAAACCAGTGACTAACCAGGTTGAGTGTACCCATACCTCACGCAGGAGAACTGATC 660
CAGTACTGCCACTCCAAGGGCATCACCGTTACGGCCTACAGCCCCCTGGGCTCTCCGGAT 720
15 AGACCTTGGGCCAAGCCAGAAGACCCTTCCCTGCTGGAGGATCCCAAGATTAAGGAGATT 780
GCTGCAAAGCACTCCCCAAGTCTGTGACACCAGCACGCATTGTTGAGAACATTCAAGTCT 840
TTGACTTTAAATTGAGTGATGAGGAGATGGCAACCATACTCAGCTTCAACAGAACTGGA 900
GGGCCTGTAACGTGTTGCAATCCTCTCATTGGAAGACTATCCCTTCGATGCAGAAATATT 960
GAGGTTGAATCTCCTGGTGAGATTATACAGGAGATTCTCTTTCTTCGCTGAAGTGTGACT 1020
20 ACCTCCACTCATGTCCCATTTTAGCCAAGCTTATTTAAGATCACAGTGAACCTTAGTCCTG 1080
TTATAGACGAGAATCGAGGTGCTGTTTTAGACATTTATTTCTGTATGTTCAACTAGGATC 1140
AGAATATCACAGAAAAGCATGGCTTGAATAAGGAAATGACAATTTTTTCCACTTATCTGA 1200
TCAGAACAAATGTTTATTAAGCATCAGAACTCTGCCAACACTGAGGATGTAAAGATCAA 1260
TAAAAAAAATAATAATCAT 1279

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SEQ ID NO: 4

	Met	Ala	Thr	Phe	Val	Glu	Leu	Ser	Thr	Lys	10
5	Ala	Lys	Met	Pro	Ile	Val	Gly	Leu	Gly	Thr	20
	Trp	Lys	Ser	Pro	Leu	Gly	Lys	Val	Lys	Glu	30
	Ala	Val	Lys	Val	Ala	Ile	Asp	Ala	Gly	Tyr	40
	Arg	His	Ile	Asp	Cys	Ala	Tyr	Val	Tyr	Gln	50
	Asn	Glu	His	Glu	Val	Gly	Glu	Ala	Ile	Gln	60
10	Glu	Lys	Ile	Gln	Glu	Lys	Ala	Val	Lys	Arg	70
	Glu	Asp	Leu	Phe	Ile	Val	Ser	Lys	Leu	Trp	80
	Pro	Thr	Phe	Phe	Glu	Arg	Pro	Leu	Val	Arg	90
	Lys	Ala	Phe	Glu	Lys	Thr	Leu	Lys	Asp	Leu	100
	Lys	Leu	Ser	Tyr	Leu	Asp	Val	Tyr	Leu	Ile	110
15	His	Trp	Pro	Gln	Gly	Phe	Lys	Ser	Gly	Asp	120
	Asp	Leu	Phe	Pro	Lys	Asp	Asp	Lys	Gly	Asn	130
	Ala	Ile	Gly	Gly	Lys	Ala	Thr	Phe	Leu	Asp	140
	Ala	Trp	Glu	Ala	Met	Glu	Glu	Leu	Val	Asp	150
	Glu	Gly	Leu	Val	Lys	Ala	Leu	Gly	Val	Ser	160
20	Asn	Phe	Ser	His	Phe	Gln	Ile	Glu	Lys	Leu	170
	Leu	Asn	Lys	Pro	Gly	Leu	Lys	Tyr	Lys	Pro	180
	Val	Thr	Asn	Gln	Val	Glu	Cys	His	Pro	Tyr	190
	Leu	Thr	Gln	Glu	Lys	Leu	Ile	Gln	Tyr	Cys	200
	His	Ser	Lys	Gly	Ile	Thr	Val	Thr	Ala	Tyr	210
25	Ser	Pro	Leu	Gly	Ser	Pro	Asp	Arg	Pro	Trp	220
	Ala	Lys	Pro	Glu	Asp	Pro	Ser	Leu	Leu	Glu	230
	Asp	Pro	Lys	Ile	Lys	Glu	Ile	Ala	Ala	Lys	240
	His	Ser	Pro	Ser	Leu						245